REMARKS

The Examiner has rejected claims 29-33 under 35 U.S.C. § 102(b) as being anticipated by the article by González et al. (1996) ("González"). The Examiner has also rejected claims 29-38 under 35 U.S.C. § 102(b) as being anticipated by the article by Puffer et al. (1997) ("Puffer"). Claim 29 stands currently amended. Claims 1-12, 17-20, and 25-28 stand previously canceled. Claims 13-16 and 21-24 stand withdrawn. Claims 13-16, 21-24, and 29-38 are currently pending. The following remarks are considered by applicant to overcome each of the Examiner's outstanding rejections to current claims 29-38. An early Notice of Allowance is therefore requested.

I. SUMMARY OF RELEVANT LAW

A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference.

II. REJECTION OF CLAIMS 29-33 UNDER 35 U.S.C. § 102(B) BASED ON GONZÁLEZ

On page 4 of the Office Action, the Examiner rejects claims 29-33 under 35 U.S.C. § 102(b) as being anticipated by González. These rejections are respectfully traversed and believed overcome in view of the following discussion.

Claim 29 states:

> "A DNA molecule comprising a nucleic acid comprising **a deletion mutation of the budding mediating motif** of a viral protein encoded by the nucleic acid,
>
> > "wherein the budding mediating motif **consists** of an amino acid sequence selected from the group consisting of PTAP (SEQ ID NO: l), PPX_1Y (SEQ ID NO:2), YX_2X_3L (SEQ ID NO:3) and a combination thereof...." (emphasis added).

González fails to disclose the deletion of a budding mediating motif consisting of any of the above three amino acid sequences or a combination thereof.

In response, Examiner cites to Fig. 1 of González as disclosing a deletion mutation of a budding mediating motif consisting of PTAP. However, as can be seen in Fig. 1 and as admitted by Examiner, the deletion is of the C-terminus which includes PTAP. In fact, Examiner admits that González discloses, in Fig. 1, a deletion of the C-terminous amino acid sequence "VETGTADKMPATSRPTAP".

As such, González discloses a deletion comprising PTAP, but not a deletion consisting of PTAP. Accordingly, González fails to disclose a deletion mutation of a budding mediating motif consisting of PTAP, as stated in Claim 29.

During a telephonic interview with the Examiner on August 14, 2008. The above was explained to the Examiner. However, it was the Examiner's position that the "comprising" language which preceded the made the claim open to deletion mutations which included the amino acids PTAP as well as amino acids which were directly adjacent to PTAP. However, Applicant's must respectfully assert that the Examiner has improperly construed the claims. More specifically, such a construction essentially reads on a deletion mutation comprising PTAP. However, Claim 29 states that it is a deletion mutation consisting of PTAP.

While Applicants respectfully disagree with the Examiner's interpretation of the claim language, Applicants have none the less amended Claim 29 so as to more explicitly clarify the "consisting" language. In particular, Applicants have amended Claim 29 to additionally state, in part:

> "wherein the budding mediating motif does **not** include of any amino acids directly adjacent to the amino acid sequence." (emphasis added).

Applicants respectfully assert that the above additional language is inherently including in the "consisting" language already present in Claim 29. Therefore, no new

limitations have been added to Claim 29. The amendment was merely made to place Claim 29 in better form, and to alleviate Examiner's concern regarding the clarity of Claim 29.

As such, Applicants respectfully assert that Examiner has failed to establish a prima facie case of anticipation of independent Claim 29, and corresponding claims 30-33 because they are each dependant from independent Claim 29. Therefore, Applicants respectfully request that Examiner remove the rejections of claims 29-33 under 35 U.S.C. § 102(b) as being anticipated by the article by González et al. (1996).

III. REJECTION OF CLAIMS 29-38 UNDER 35 U.S.C. § 102(B) BASED ON PUFFER

On page 5 of the Office Action, the Examiner rejects claims 29-38 under 35 U.S.C. § 102(b) as being anticipated by Puffer. These rejections are respectfully traversed and believed overcome in view of the following discussion.

Claim 29-33

Claim 29 states, in part:

> "A DNA molecule comprising a nucleic acid comprising **a deletion mutation of the budding mediating motif** of a viral protein encoded by the nucleic acid,
>
> > "wherein the budding mediating motif **consists** of an amino acid sequence selected from the group consisting of PTAP (SEQ ID NO: 1), PPX_1Y (SEQ ID NO:2), YX_2X_3L (SEQ ID NO:3) and a combination thereof...." (emphasis added).

Puffer fails to disclose the deletion of a budding mediating motif consisting of any of the above three amino acid sequences or a combination thereof.

Examiner cites to the abstract, page 6542 (left column – "Materials and Methods"), and Fig. 1 of Puffer as disclosing a deletion mutation of a budding mediating motif consisting of YX_2X_3L. However, this misinterprets the teachings of Puffer.

Puffer states that "the L domain in EIAV p9 utilizes a YXXL motif". Puffer, Abstract. Puffer later goes on to state that the L domain of EIAV can be replaced with the L

domains of HIV-1 P6 and RSV p2b. Puffer, P. 6542, left column. As such, Puffer relates to a substitution mutation of YXXL, and not a deletion mutation. Moreover, Puffer states that what was done was that the p9 residues Q^{20}, N^{21}, L^{22}, Y^{23}, P^{24}, D^{25}, L^{26}, S^{27}, E^{28}, I^{29}, and K^{30} were individually changed to alanine. Puffer, P. 6544, right column (under heading "Characterization of critical residues within the EIAV L domain"). Thus, not only does Puffer relate to a substitution mutation instead of a deletion mutation, but Puffer only relates to changing out individual amino acids, and not an amino acid sequence. Further, all of Puffers later discussion of YXXL is in terms of "suggested" functions and "hypothesis". This is a far cry from disclosing a deletion mutation of a budding mediating motif consisting of YXXL. Accordingly, Puffer fails to disclose a deletion mutation of a budding mediating motif consisting of YX_2X_3L, as stated in Claim 29.

As such, Applicants respectfully assert that Examiner has failed to establish a prima facie case of anticipation of independent Claim 29, and corresponding claims 30-33 because they are each dependant from independent Claim 29. Therefore, Applicants respectfully request that Examiner remove the rejections of claims 29-33 under 35 U.S.C. § 102(b) as being anticipated by the article by Puffer et al. (1997).

Claim 34-38

Claim 34 states, in part:

> "A DNA molecule comprising a nucleic acid comprising **a deletion mutation of the budding mediating motif** of a viral protein encoded by the nucleic acid,
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> ***
>
> "wherein the budding mediating motif **comprises** an amino acid sequence selected from the group consisting of PPX_1Y (SEQ ID NO:2), YX_2X_3L (SEQ ID NO:3) and a combination thereof...." (emphasis added).

None of the references to which the Examiner cites disclose a budding mediating motif comprising either PPX_1Y, where X_1 is not P, or YX_2X_3L.

Puffer fails to disclose the deletion of a budding mediating motif comprising any of the above three amino acid sequences or a combination thereof.

Examiner cites to the abstract, page 6542 (left column – "Materials and Methods"), and Fig. 1 of González as disclosing a deletion mutation of a budding mediating motif comprising YX_2X_3L. However, this misinterprets the teachings of Puffer.

Puffer states that "the L domain in EIAV p9 utilizes a YXXL motif". Puffer, Abstract. Puffer later goes on to state that the L domain of EIAV can be replaced with the L domains of HIV-1 P6 and RSV p2b. Puffer, P. 6542, left column. As such, Puffer relates to a substitution mutation of YXXL, and not a deletion mutation. Moreover, Puffer states that what was done was that the p9 residues Q^{20}, N^{21}, L^{22}, Y^{23}, P^{24}, D^{25}, L^{26}, S^{27}, E^{28}, I^{29}, and K^{30} were individually changed to alanine. Puffer, P. 6544, right column (under heading "Characterization of critical residues within the EIAV L domain"). Thus, not only does Puffer relate to a substitution mutation instead of a deletion mutation, but Puffer only relates to changing out individual amino acids, and not an amino acid sequence. Further, all of Puffers later discussion of YXXL is in terms of "suggested" functions and "hypothesis". This is a far cry from disclosing a deletion mutation of a budding mediating motif comprising YXXL. Accordingly, Puffer fails to disclose a deletion mutation of a budding mediating motif comprising YX_2X_3L, as stated in Claim 29.

As such, Applicants respectfully assert that Examiner has failed to establish a prima facie case of anticipation of independent Claim 34, and corresponding claims 35-38 because they are each dependant from independent Claim 34. Therefore, Applicants respectfully request that Examiner remove the rejections of claims 34-38 under 35 U.S.C. § 102(b) as being anticipated by the article by Puffer et al. (1997).

Based upon the above remarks, Applicants respectfully request reconsideration of this application and its early allowance. Should the Examiner feel that a telephone conference

with Applicants' attorney would expedite the prosecution of this application, the Examiner is urged to contact him at the number indicated below.

Respectfully submitted,

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